AMENDMENTS TO THE CLAIMS

1. (Currently amended) A method of identifying a genetic ~~mutations~~ mutation that [[are]] is associated with adult onset cerebellar ataxia in a human subject, said method comprising:

(a) determining a first nucleic acid sequence of a human protein kinase C gamma gene from a first human subject exhibiting adult onset cerebellar ataxia;

(b) ~~identifying~~ comparing the first nucleic acid sequence to SEQ ID NO:3 to identify a difference between the first nucleic acid sequence from the first human subject exhibiting adult onset cerebellar ataxia and SEQ ID NO:3, wherein the difference alters the amino acid sequence encoded by the human protein kinase C gamma gene; and

(c) confirming that the difference identified between the first nucleic acid sequence and SEQ ID NO:3 is a genetic mutation associated with adult onset cerebellar ataxia by co-segregation analysis ~~comprising determining that the identified nucleic acid sequence difference is also present in a plurality of human subjects exhibiting adult onset cerebellar ataxia and is absent in a plurality of human subjects not exhibiting adult onset cerebellar ataxia~~.

2. (Previously presented) The method of Claim 1 wherein the first nucleic acid sequence from said first human subject is determined by amplification of at least a portion of the human protein kinase C gamma gene from genomic DNA isolated from said human subject to produce an amplified DNA and sequencing said amplified DNA.

3. (Canceled)

4. (Currently amended) The method of Claim 1 wherein said co-segregation analysis comprises a method selected from the group consisting of direct sequencing, sequencing

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CHRISTENSEN O'CONNOR JOHNSON KINDNESS PLLC
1420 Fifth Avenue
Suite 2800
Seattle, Washington 98101
206.682.8100

PCR-amplified DNA, single stranded conformation analysis, allele-specific PCR and restriction fragment length polymorphism analysis.

5. (Previously presented) The method of Claim 4 wherein said co-segregation analysis comprises sequencing PCR-amplified DNA.

6. (Previously presented) The method of Claim 4 wherein said co-segregation analysis comprises restriction fragment length polymorphism analysis.

7-42. (Canceled)

43. (Previously presented) The method of Claim 1, wherein the first nucleic acid sequence is a coding region of the human protein kinase C gamma gene selected from the group consisting of exon 1; exon 2; exon 3; exon 4; exon 5; exon 6; exon 7; exon 8; exon 9; exon 10; exon 11; exon 12; exon 13; exon 14; exon 15; exon 16; exon 17; and exon 18.

44. (Previously presented) The method of Claim 1, wherein the first nucleic acid sequence comprises exon 4 of the human protein kinase C gamma gene.

45. (Previously presented) The method of Claim 1, wherein the mutation associated with adult onset cerebellar ataxia is selected from the group consisting of a missense mutation, a deletion mutation, and an insertion mutation.

46. (Previously presented) The method of Claim 45, wherein the mutation is a missense mutation.

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1420 Fifth Avenue
Suite 2800
Seattle, Washington 98101
206.682.8100